



SEQUENCE LISTING

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<120> Novel 35 kD Protein

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<140> 10/511,270

<141> 2005-05-23

<150> PCT/JP03/05431

<151> 2003-04-20

<150> Japan 2002-126107

<151> 2002-04-26

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<170> PatentIn version 3.3

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<211> 1061

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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Ser	Arg	Ser	Leu	Ser	Arg	Asn	Val	Gly	Val	Trp	Ala	Ser	Gly	Glu	Gly	
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Lys	Lys	Val	Asp	Ile	Ala	Gly	Ile	Tyr	Pro	Pro	Val	Thr	Thr	Pro	Phe	
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aaa	ctg	ggc	acc	ttc	ccc	ttc	cga	ggc	ttc	gtg	gtc	cag	ggc	tcc	aat	241
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Gly Cys Glu Ser Thr Gln Ala Thr Val Glu Met Thr Val Ser Met Ala	
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Gln Val Gly Ala Asp Ala Ala Met Val Val Thr Pro Cys Tyr Tyr Arg	
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Gly Arg Met Ser Ser Ala Ala Leu Ile His His Tyr Thr Lys Val Ala	
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Asp Leu Ser Pro Ile Pro Val Val Leu Tyr Ser Val Pro Ala Asn Thr	
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Gly Leu Asp Leu Pro Val Asp Ala Val Val Thr Leu Ser Gln His Pro	
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Asn Ile Val Gly Met Lys Asp Ser Gly Gly Asp Val Thr Arg Ile Gly	
195 200 205	
ctg att gtt cac aag acc agg aag cag gat ttt cag gtg ttg gct gga	673
Leu Ile Val His Lys Thr Arg Lys Gln Asp Phe Gln Val Leu Ala Gly	
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Ser Ala Gly Phe Leu Met Ala Ser Tyr Ala Leu Gly Ala Val Gly Gly	
225 230 235	
gtc tgc gcc ctg gcc aat gtc ctg ggg gct cag gtg tgc cag ctg gag	769
Val Cys Ala Leu Ala Asn Val Leu Gly Ala Gln Val Cys Gln Leu Glu	
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cga ctg tgc tgc acg ggg caa tgg gaa gat gcc cag aaa ctg cag cac	817
Arg Leu Cys Cys Thr Gly Gln Trp Glu Asp Ala Gln Lys Leu Gln His	
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Thr Ala Glu Val Asp Tyr Gly Lys Leu Glu Glu Asn Leu His Lys Leu
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Gly Thr Phe Pro Phe Arg Gly Phe Val Val Gln Gly Ser Asn Gly Glu
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Phe Pro Phe Leu Thr Ser Ser Glu Arg Leu Glu Val Val Ser Arg Val
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Arg Gln Ala Met Pro Lys Asn Arg Leu Leu Leu Ala Gly Ser Gly Cys
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Glu Ser Thr Gln Ala Thr Val Glu Met Thr Val Ser Met Ala Gln Val
 115 120 125

Gly Ala Asp Ala Ala Met Val Val Thr Pro Cys Tyr Tyr Arg Gly Arg
 130 135 140

Met Ser Ser Ala Ala Leu Ile His His Tyr Thr Lys Val Ala Asp Leu
 145 150 155 160

Ser Pro Ile Pro Val Val Leu Tyr Ser Val Pro Ala Asn Thr Gly Leu
 165 170 175

Asp Leu Pro Val Asp Ala Val Val Thr Leu Ser Gln His Pro Asn Ile
 180 185 190

Val Gly Met Lys Asp Ser Gly Gly Asp Val Thr Arg Ile Gly Leu Ile
 195 200 205

Val His Lys Thr Arg Lys Gln Asp Phe Gln Val Leu Ala Gly Ser Ala
 210 215 220

Gly Phe Leu Met Ala Ser Tyr Ala Leu Gly Ala Val Gly Gly Val Cys
 225 230 235 240

Ala Leu Ala Asn Val Leu Gly Ala Gln Val Cys Gln Leu Glu Arg Leu
 245 250 255

Cys Cys Thr Gly Gln Trp Glu Asp Ala Gln Lys Leu Gln His Arg Leu
 260 265 270

Ile Glu Pro Asn Ala Ala Val Thr Arg Arg Phe Gly Ile Pro Gly Leu
 275 280 285

Lys Lys Ile Met Asp Trp Phe Gly Tyr Tyr Gly Gly Pro Cys Arg Ala
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Phe Thr Ser Asn Gly Trp Leu
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 Ser Arg Gly Leu Ser Arg Asn Val Lys Gly Lys Lys Ile Asp Ile Ala
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 ggc atc tac cca ccc gtg acc acc cca ttc acc gcc acc gca gaa gta 146
 Gly Ile Tyr Pro Pro Val Thr Thr Pro Phe Thr Ala Thr Ala Glu Val
 35 40 45
 gac tat ggg aaa ctg gaa gag aac ctg aac aaa ctg gcc gcc ttc ccc 194
 Asp Tyr Gly Lys Leu Glu Glu Asn Leu Asn Lys Leu Ala Ala Phe Pro
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ccc	aag	gac	aag	ctc	ctg	ata	gcc	ggc	tct	ggc	tgc	gag	tcc	acg	caa	338	
Pro	Lys	Asp	Lys	Leu	Leu	Ile	Ala	Gly	Ser	Gly	Cys	Glu	Ser	Thr	Gln		
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Ala	Thr	Val	Glu	Met	Thr	Val	Ser	Met	Ala	Gln	Val	Gly	Ala	Asp	Ala		
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gtg	gtg	ctg	tac	agt	gtc	cca	ggc	aac	acg	ggg	cta	gag	ctg	cct	gtg	530	
Val	Val	Leu	Tyr	Ser	Val	Pro	Gly	Asn	Thr	Gly	Leu	Glu	Leu	Pro	Val		
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gat	gcc	gtg	gtc	aca	ttg	tct	cag	cac	cca	aat	atc	att	ggc	ttg	aag	578	
Asp	Ala	Val	Val	Thr	Leu	Ser	Gln	His	Pro	Asn	Ile	Ile	Gly	Leu	Lys		
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Asp	Ser	Gly	Gly	Asp	Val	Thr	Arg	Thr	Gly	Leu	Ile	Val	His	Lys	Thr		
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275					280					285							
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305					310					315							

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 35 40 45

Gly Lys Leu Glu Glu Asn Leu Asn Lys Leu Ala Ala Phe Pro Phe Arg
 50 55 60

Gly Phe Val Val Gln Gly Ser Thr Gly Glu Phe Pro Phe Leu Thr Ser
 65 70 75 80

Leu Glu Arg Leu Glu Val Val Ser Arg Val Arg Gln Ala Ile Pro Lys
 85 90 95

Asp Lys Leu Leu Ile Ala Gly Ser Gly Cys Glu Ser Thr Gln Ala Thr
 100 105 110

Val Glu Met Thr Val Ser Met Ala Gln Val Gly Ala Asp Ala Ala Met
 115 120 125

Val Val Thr Pro Cys Tyr Tyr Arg Gly Arg Met Asn Ser Ala Ala Leu
 130 135 140

Ile His His Tyr Thr Lys Val Ala Asp Leu Ser Pro Ile Pro Val Val
 145 150 155 160

Leu Tyr Ser Val Pro Gly Asn Thr Gly Leu Glu Leu Pro Val Asp Ala
 165 170 175

Val Val Thr Leu Ser Gln His Pro Asn Ile Ile Gly Leu Lys Asp Ser
 180 185 190

Gly Gly Asp Val Thr Arg Thr Gly Leu Ile Val His Lys Thr Ser Lys
 195 200 205

Gln Asp Phe Gln Val Leu Ala Gly Ser Val Gly Phe Leu Leu Ala Ser
 210 215 220

Tyr Ala Val Gly Ala Val Gly Gly Ile Cys Gly Leu Ala Asn Val Leu
 225 230 235 240

Gly Ala Gln Val Cys Gln Leu Glu Arg Leu Cys Leu Thr Gly Gln Gly
 245 250 255

Glu Ala Ala Gln Arg Leu Gln His Arg Leu Ile Glu Pro Asn Thr Ala
 260 265 270

Val Thr Arg Arg Phe Gly Ile Pro Gly Leu Lys Lys Thr Met Asp Trp
 275 280 285

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35 40 45

Asn Ile Ile Gly Leu Lys Asp Ser Gly Gly Asp Val Thr Arg Thr Gly
50 55 60

Leu Ile Val His Lys Thr Ser Lys Gln Asp Phe Gln Val Leu Ala Gly
65 70 75 80

Ser Val Gly Phe Leu Leu Ala Ser Tyr Ala Val Gly Ala Val Gly Gly
85 90 95

Ile Val Gly Leu Ala Asn Val Leu Gly Ala Gln Val Cys Gln Leu Glu
100 105 110

Arg Leu Cys Leu Thr Gly Gln Gly Glu Ala Ala Gln Arg Leu Gln His
115 120 125

Arg Leu Ile Glu Pro Asn Thr Ala Val Thr Arg Arg Phe Gly Ile Pro
130 135 140

Gly Leu Lys Lys Thr Met Asp Trp Phe Gly Tyr Tyr Gly Gly Pro Cys
145 150 155 160

Arg Ala Pro Leu Xaa Glu Leu Ser Pro Ser Glu Glu Glu Ala Leu Arg
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